

OM protein - nucleic search, using frame_plus_p2n model

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Run on:      May 26, 2004, 08:40:32 ; Search time 16 Seconds
              (without alignments)
              2.323 Million cell updates/sec
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```

Title:          us-09-989-730-401
Perfect score:  993
Sequence:       1 MEVPALCLLWALAMVTPAS.....AQQHRLROIQRULTAALPA 198

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Scoring table:	BLOSUM62	
	Xgapop 10.0 ,	Xgapext 0.5
	Ygapop 10.0 ,	Ygapext 0.5
	Zgapop 6.0 ,	Zgapext 7.0
	Delop 6.0 ,	Delext 7.0

Searched: 45 seqs, 93847 residues
Total number of hits satisfying chosen parameters: 90

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 s

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Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=us-09-989-730-401 -DB=rni401.seq
-SUFFIX=pto -OUT=us-09-989-730-401.rni -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLPHY -NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : rni401.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	897.5	90.4	990	1	US-09-369-247-16 Sequence 16, Appl

RESULT 1
US-09-369-247-16
; Sequence 16, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 16
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-369-247-16

Alignment Scores:

Needham	0	Length:	990
Pred. No.:	897.50	Matches:	193
Score:	82.55%	Conservative:	1
Percent Similarity:	82.13%	Mismatches:	4
Best Local Similarity:	90.38%	Indels:	39
Query Match:	1	Gaps:	1
DB:			

us-09-989-730-401 (1-198) x US-09-369-247-16 (1-990)

Qy	1	MetProValProAlaLeuCysLeuLeuTrpAlaLeuAlaMetValThrArgProAlaSer	20
Db	3	ATGCCAGTGCCTACTCTGTGCTGCTGTGGGCCCTGGCAATGGTGACCCCGGCCTGCCTCA	62
Qy	21	AlaAlaProMetGlyGlyProGluLeuAlaGlnHisGluGluLeuThrLeuLeuPheHis	40
Db	63	CGGGCCCCCATGGSCGGCCAGAACTGGCACAGCATGAGAGAGCTGACCCCTGCTCTTCCAC	122

Appendix A

us-09-989-730-401.rni

QY	41	GlyThrLeuGlnLeuGlyGlnAlaLeuAsnGlyValTyrArgThrThrGluGlyArgLeu	60
Db	123	GGGACCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGAGCGCTG	182
QY	61	ThrLysAlaArgAsnSerLeuGlyLeuTyrGlyArgThrIleGluLeuLeuGlyGlnGlu	80
Db	183	ACAAAGGCCAGGAACAGCCTGGGTCTCTATGGCCGCCACAATAGAACTCCTGGGGCAGGAG	242
QY	81	ValSerArgGlyArgAspAlaAlaGlnGluLeuArgAlaSerLeuLeuGluThrGlnMet	100
Db	243	GTCAAGCGGGGCCGGGATGCAGCCCAAGAACTTCGGGCAAGCCTGTGGAGACTCAGATG	302
QY	101	GluGluAspIleLeuGlnLeuGlnAlaGluAlaThrAlaGluValLeuGlyGluValAla	120
Db	303	GAGGAGGATATTCTGCAGCTGCAGGCAGGAGGCCACAGCTGAGGTGCTGGGGAGGTGGCC	362
QY	121	GlnAlaGlnLysValLeuArgAspSerValGlnArgLeuGluValGlnLeuArgSerAla	140
Db	363	CAGGCACAGAGGTGCTACGGGACAGCGTKCAGCGGCTAGAGTCCAGYTRAGAGGCC	422
QY	141	TrpLeuGlyProAlaTyrArgGluPheGluValLeuLysAlaHisAlaAspLysGln--S	160
Db	423	TGGCTGGGCCCTGCCCTACCGAGATTGAGGTTTAAAGGCTCAGGCTGACAGCAAGAG	482
QY	160	erHisIleLeuTrpAlaLeuThrGlyHisValGlnArgGlnArgGluMetValAlaG	180
Db	483	CCACATCCTATGGCC-CTCACAGGCCACGT-CAGCGGCAGAGCGGGAGATGGTGGCAC	540
QY	180	lnGlnHisArgLeuArgGlnIleGlnGlu-----	189
Db	541	AGCAGCATCGGCTGCGACAGATCCAGGAGAGGTGAGCCTGGCAGGGGTTTGGCAGGCAGG	600
QY	189	-----	189
Db	601	GCAGTTGGATGGGGGGCGCACAGGGCAGCTGGAAAGGGGCCCTCACCTGGGCTGAGCC	660
QY	190	-----ArgLeuHisThrAlaAlaLeuProAla	198
Db	661	ACATCTCCCTCCCCAGACTCCACACAGCGGGCGCTCCAGCC	701

OM protein - nucleic search, using frame plus p2n model

Run on: May 26, 2004, 08:40:32 ; Search time 16 Seconds
(without alignments) 2.323 Million cell updates/sec

```

Title:          us-09-989-730-401
Perfect score:  993
Sequence:       1 MPVPALCLLWALAMVTRPAS.....AQQHRLROIQERLHTAALPA 198

```

Scoring table:

BLOSUM62	
Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delopop 6.0 ,	Delext 7.0

Searched: 45 seqs, 93847 residues
Total number of hits satisfying chosen parameters: 90

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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Command line parameters:
-MODEL=frame+p2n.model -DEV=soft -Q=us-09-989-730-401 -DB=rni401.seq
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-UNITS=bits -START=1 -END=-1 -MATRIX=blossum2 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLPXY -NEG_SCORES=0 -LONGLOG -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : rmi401.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	897.5	90.4	990	1	US-09-369-247-16	Sequence 16, Appl

Alignment Scores:	
Pred. No.:	0
Score:	897.50
Percent Similarity:	82.55%
Best Local Similarity:	82.13%
Query Match:	90.38%
DB:	1
Length:	990
Matches:	193
Conservative:	1
Mismatches:	4
Indels:	39
Gaps:	1

u8-09-989-730-401 (1-198) x US-09-369-247-16 (1-990)

Qy		1	MetProValProAlaLeuCysLeuLeuTtpAlaLeuAlaMetValThrArgProAlaSer	20
Db		3	ATGCCAGTGCCCTACTGTGCGCTGCTGTGGGCCCTGGCAATGGTGACCCGGGCCTGCCTCA	52
Qy		21	AlaAlaProMetGlyGlyProGluLeuAlaGlnHisGluGluLeuThrLeuLeuPheHis	40
Db		63	GCGGCCCCCATTGGSCGSCCAGAACTGGCACAGCATGAGAGACTGACCCCTGCTCTTCAC	128

Appendix A

us-09-989-730-401.rni

```
QY 41 GlyThrLeuGlnLeuGlyGlnAlaLeuAsnGlyValTyrArgThrThrGluGlyArgLeu 60
Db 123 GGGACCTGCGAGCTGGGCGAGGCCCTCAACGGTGTGTACAGGACCACGGAGGCGGCTG 182

QY 61 ThrLysAlaArgAsnSerLeuGlyLeuTyrGlyArgThrIleGluLeuLeuGlyGlnGlu 80
Db 183 ACNAAAGGCCAGGAACAGCCTGGGTCTCTATGGCCGCGACAAATAGAACTCCTGGGGCAGGAG 242

QY 81 ValSerArgGlyArgAspAlaAlaGlnGlnLeuArgAlaSerLeuLeuGluThrGlnMet 100
Db 243 GTCAGCCGGGGCCGGGATGCGAGCCAGGAACTTCGGCAAGCCTGTTGGAGACTCAGATG 302

QY 101 GluGluAspIleLeuGlnLeuGlnAlaGluAlaThrAlaGluValLeuGlyGluValAla 120
Db 303 GAGGAGGATATTCTCGAGCTGCAGGCGAGGCGCACAGCTGAGGTGCTGGGGAGGTGGCC 362

QY 121 GlnAlaGlnLysValLeuArgAspSerValGlnArgLeuGluValGlnLeuArgSerAla 140
Db 363 CAGGCACAGAAGGTGTACGGGACAGCGTTCAGCGGCTAGAGTCCAGYTRAGAGCGCC 422

QY 141 TrpLeuGlyProAlaTyrArgGluPheGluValLeuLysAlaHisAlaAspLysGln--S 160
Db 423 TGGCTGGGCCCCCTGCCTACCGAGAATTGAGGTCTTAAAGGCTCAGCTGACAAAGCAAGAG 482

QY 160 exHisIleLeuTyrAlaLeuThrGlyHisValGlnArgGlnArgGluMetValAlaG 180
Db 483 CCCACATCCTATGGCC-CTCACAGGCCACGT-CAGCGGCAGAGCGGGAGATGCTGGCAC 540

QY 180 InGlnHisArgLeuArgGlnIleGlnGlu----- 189
Db 541 AGCAGCATCGGCTGCGACAGATCCAGGAGAGGTGAGCCTGGCAGGGGTTTGGCAGGCAGG 600

QY 189 ----- 189
Db 601 GCAGTTGGATGGGGGGCGGCACAGGGCAGCTGGAAAGGGGCCCCCTCACCTGGGCTGAGCC 660

QY 190 -----ArgLeuHisThrAlaAlaLeuProAla 198
Db 661 ACATCTCCCTCCCCAGACTCCACACAGCGGGCGCTCCAGCC 701
```

Appendix B

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 08:17:52 ; Search time 73 Seconds
(without alignments)
4.114 Million cell updates/sec

Title: us-09-989-730-400
Perfect score: 893
Sequence: 1 gtcagccagtgctgctct.....aaaaaaaaaaaaaaaaaaaa 893

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 45 seqs, 168143 residues

Total number of hits satisfying chosen parameters: 90

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : rni400.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	84.9	990	1	US-09-369-247-16
					Sequence 16, Appl

RESULT 1
US-09-369-247-16
; Sequence 16, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
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; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-369-247-16

Query Match 84.9%; Score 758; DB 1; Length 990;
Best Local Similarity 86.9%; Pred. No. 3.6e-16;
Matches 855; Conservative 8; Mismatches 13; Indels 108; Gaps 4;

QY	3	CATGCCAGTGCCTGCTCTGTGCTGCTCTGTGSCCTGGCAATGTTGACCCGCTGCTC	62
Db	2	CATGCCAGTGCCTGCTCTGTGCTGCTGCTGTGSCCTGGCAATGTTGACCCGCTGCTC	61
QY	63	AGCGGCCCCCATGGGCGGCCCCAGAACTGGCCACAGCATGAGGAGCTGACCTGCTCTTCCA	122
Db	62	AGCGGCCCCCATGGGCGGCCCCAGAACTGGCCACAGCATGAGGAGCTGACCTGCTCTTCCA	121
QY	123	TGGGACCCCTGCAGCTGGGCGGCCCCCTCAACGGTGTGTACAGGACCACGAGGGACGGCT	182
Db	122	CGGACCCCTGCAGCTGGGCGGCCCCCTCAACGGTGTGTACAGGACCACGAGGGACGGCT	181
QY	183	GACAAAGGCCAGGAACAGCTGGTCTCTATGGCCGCAACATAGAACTCTGGGGCAGGA	242
Db	182	GACAAAGGCCAGGAACAGCTGGTCTCTATGGCCGCAACATAGAACTCTGGGGCAGGA	241
QY	243	GGTCAGCCGGGGCCGGGATGTCAGCCAGGAACCTGGGCAAGCCTGTTGAGACTCAGAT	302
Db	242	GGTCAGCCGGGGCCGGGATGTCAGCCAGGAACCTGGGCAAGCCTGTTGAGACTCAGAT	301
QY	303	GGAGGAGGATATTCTGCACTGCAGGTCAGGCGAGGCGACAGCTGAGGTGCTGGGGAGGTGGC	362
Db	302	GGAGGAGGATATTCTGCACTGCAGGTCAGGCGAGGCGACAGCTGAGGTGCTGGGGAGGTGGC	361

us-09-989-730-400.rni

363	Qy	CCAGGCACAGAAAGGTGCTACCGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGC	422
362	Db	CCAGGCACAGAAAGGTGCTACCGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGC	421
423	Qy	CTGGCTGGGCCCTGCTACCGAGAAATTGAGGTCTTAAAGGCTCACGCTGACAAAGC-AGA	481
422	Db	CTGGCTGGGCCCTGCTACCGAGAAATTGAGGTCTTAAAGGCTCACGCTGACAAAGCAAGA	481
482	Qy	GCCACATCCTATGGGGCCCTCACAGGCCACGTCGACGGGCAGAGCGGGGAGATGCTGGCAC	541
482	Db	GCCACATCCTATGGGGCCCTCACAGGCCACGT-CAGCGGCAGAGCGGGGAGATGCTGGCAC	540
542	Qy	AGCAGCATCGGCTGCGACAGATCCAGGAG-----	570
541	Db	AGCAGCATCGGCTGCGACAGATCCAGGAGGTGAGCCTGGCAGGGGTTTGGCAGGCAGG	600
571	Qy	-----	570
601	Db	GCAGTTGGATGGGGGGCGGCACAGGGCAGCTGGAAGGGGCCCCCTCACCTGGGCTGAGCC	660
571	Qy	-----AGACTCCACACAGCGGGCGTCCAGCCTGAATCTGCCTGGATGGAA	616
661	Db	ACATCTCCCTCCCGAGACTCCACACAGCGGGCGTCCAGCCTGAATCTGCCTGGATGGAA	720
617	Qy	CTGAGGACCAATCATGCTGCAAGGAACACTTCCACGCCCGGTGAGGCCCTGTGCAGGGA	676
721	Db	CTGAGGACCAATCATGCTGCAAGGAACACTTCCAGGCCCGGTGAGGCCCTGTGCAGGGA	780
677	Qy	GGAGCTGCCTGTTCACTGGGATCAGCCAGGGCGCGGGGCCCCACCTTCTGAGCACAGAGCA	736
781	Db	GGAGCTGCSTGTTCACTGGGAYMAGCCAGGGCGCGGGGCCCCACCTTCTGAGCACAGAGCA	840
737	Qy	GAGACAGACGCGAGCGGGGGAACAAGGCAGAGGATGTAG-CCCCATTGGGGAGGGTGGAG	795
841	Db	GAGACAGACGCGAGCGGGGGAACAAGGCAGAGGATGTAGTCCCCATTGGGGAGGGTGGAG	900
796	Qy	GAGGACATGTACCCTTTTCATGCCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTTC	855
901	Db	GAGGACATGTACCCTTTTCATGCCCTACACACCCCTCATTAAGCAGAGTCGTGGCATCTC	960
856	Qy	AAAAAAAAAAAAAAAAAAAAA	879
961	Db	AAAAAAAAAAAAAAAAAAAAA	984

4.114 Million cell updates/sec

Result	Query	Score	Match	Length	DB	ID	Description
1	758	84.9	990	1	US-09-369-247-16		Sequence 16, Appo

QY	3	CATGCCAGTGCCCTGCTCTGTGTGCCTGCTCTGGGCCCTGGCAATGGTACCCGGCCCTGCCTC	62
Db	2	CATGCCAGTGCCCTACTCTGTGTGCCTGCTGTGGGCCCTGGCAATGGTACCCGGCCCTGCCTC	61
QY	63	AGCGGCCCCCATGGGGGCCCCAGAACTGGCCACAGCATGAGGAGCTGACCTGCTCTTCCCA	122
Db	62	AGCGGCCCCCATGGSCGGGCCCCAGAACTGGCCACAGCATGAGGAGCTGACCTGCTCTTCCCA	121
QY	123	TGGGACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCCACGGAGGGACGGCT	182
Db	122	CGGGACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCCACGGAGGGACGGCT	181
QY	183	GACAAAGGCCAGGAACAGCCTTGGGTCTCTATGSCCGCACAAATAGAACTCTCTGGGGCAGGA	242
Db	182	GACAAAGGCCAGGAACAGCCTGGGTCTCTATGSCCGCACAAATAGAACTCTCTGGGGCAGGA	241
QY	243	GGTCAGCCGGGGCCGGGATGCAGGCCAGGAACCTTCGGGGCAAGCCTGTGTGGAGACTCAGAT	302
Db	242	GGTCAGCCGGGGCCGGGATGCAGGCCAGGAACCTTCGGGGCAAGCCTGTGTGGAGACTCAGAT	301
QY	303	GGAGGAGGATATTCTGCAGCTGCAGGCCAGGGCCACAGCTGAGGTGCTGGGGGAGGTGGC	362
Db	302	GGAGGAGGATATTCTGCAGCTGCAGGCCAGGGCCACAGCTGAGGTGCTGGGGGAGGTGGC	361

Appendix B

us-09-989-730-400.rni

QY	363	CCAGGCACAGAAGGTGCTACGGGACAGCGGTGACGGGCTAGAGTCCAGCTGAGGAGCGC	422
Db	362		
QY	423	CTGGCTGGGCGCTGCTACCGGAGGATTTGAGGTCTTAAAGGCTCAGGCTGACAAGC-AGA	481
Db	422		
QY	482	GCCACATCTATGGGCGCTCAGGCGCACGTCAGCGGACAGAGCGGGAGATGTTGGCAC	541
Db	482		
QY	542	AGCAGCATCGGCTGCGACAGATCCAGGAG-	570
Db	541		
QY	571	-----	570
Db	601	GCAGTTGGATGGGGCGGCACAGGCGAGCTGGAAGGGGCGCCCTCACCTGGGCTGAGCC	660
QY	571	-----AGACTCCACACAGCGGGCGCTCCAGGCTGAATCTGGCTGGATGGAA	616
Db	661		
QY	617	CTGAGGACCAATCATGCTGCAAGGAACACTTCCAGCGCGCGGTGAGGCCCTGTGCGAGGGA	676
Db	721		
QY	677	GGAGCTGCTGTTCACTGGGATCAGCGGCGCGCGGCGCCCACTTCTGAGCACAGAGCA	736
Db	781		
QY	737	GAGACAGACGCGGCGGGGACAAAGGACAGAGATGTAG-CCCCATTGGGGAGGGTGGAG	795
Db	841		
QY	796	GAAGGACATGTACCTTTTCATGCTACACACCCCTCATTAAGCAGAGTCTGGGCTTTC	855
Db	901		
QY	856	AAAAAAAAAAAAAAAAAAAAA	879
Db	961	AAAAAAAAAAAAAAAAAAAAA	984